

CLAIMS:

1. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence having homology to a regulator of gene expression or a derivative of said gene regulator.
2. An isolated nucleic acid molecule according to claim 1 wherein the regulator comprises a zinc finger domain of an (HC₃)₂ type.
3. An isolated nucleic acid molecule according to claim 2 wherein the sequence of nucleotides or complementary sequence of nucleotides is selected from:
 - (i) a nucleotide sequence set forth in SEQ ID NO:2;
 - (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:3;
 - (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
 - (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).
4. An isolated nucleic acid molecule according to claim 1 wherein said gene regulator is a guanine nucleotide exchange factor (GEF) or a derivative thereof.
5. An isolated nucleic acid molecule according to claim 4 wherein the sequence of nucleotides is selected from:
 - (i) a nucleotide sequence set forth in SEQ ID NO:4 or 6;
 - (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:5 or 7;
 - (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
 - (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the

nucleotide sequence set forth in (i), (ii) or (iii).

6. An isolated nucleic acid molecule according to claim 1, wherein said gene regulator is a heat shock protein or is a heat shock binding protein or a derivative thereof.

7. An isolated nucleic acid molecule according to claim 6, wherein the sequence of nucleotides is selected from:

- (i) a nucleotide sequence set forth in SEQ ID NO:8;
- (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:9;
- (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
- (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).

8. A genetic construct comprising a vector portion and a gene portion comprising a regulator of gene expression or a derivative thereof.

9. A genetic construct according to claim 8 wherein the gene portion comprises a zinc finger domain of $(HC_3)_2$ type.

10. A genetic construct according to claim 9 wherein the gene portion comprises a nucleotide sequence selected from:

- (i) a nucleotide sequence set forth in SEQ ID NO:2;
- (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:3;
- (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
- (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).

11. A genetic construct according to claim 8 wherein said gene portion is a nucleotide exchange factor (GEF) or derivative thereof.

12. A genetic construct according to claim 11 wherein the gene portion comprises a nucleotide sequence selected from:

- (i) a nucleotide sequence set forth in SEQ ID NO:4 or 6;
- (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:5 or 7;
- (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
- (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).

13. A genetic construct according to claim 8 wherein the gene portion is a heat shock protein or a derivative thereof or a heat shock binding protein or derivative thereof.

14. A genetic construct according to claim 13 wherein the gene portion comprises a nucleotide sequence selected from:

- (i) a nucleotide sequence set forth in SEQ ID NO:8;
- (ii) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:9;
- (iii) a nucleotide sequence having at least about 40% similarity to the nucleotide sequence of (i) or (ii); and
- (iv) a nucleotide sequence capable of hybridising under low stringency conditions to the nucleotide sequence set forth in (i), (ii) or (iii).

15. A nucleic acid molecule encoding a gene regulator having the identifying characteristics of a molecule selected from MCG4, MCG7 and MCG18 having respective amino acid sequences of SEQ ID NO:3, SEQ ID NO: 5 or 7 and SEQ ID NO:9.

16. A method of detecting a condition caused or facilitated by an aberration in *mcg4*, said method comprising determining the presence of a single or multiple nucleotide substitution, deletion and/or addition or other aberration to one or both alleles of said *mcg4* wherein the presence of such a nucleotide substitution, deletion and/or addition or other aberration may be indicative of said condition or a propensity to develop said condition.

17. A method of detecting a condition caused or facilitated by an aberration in *mcg4*, said method comprising screening for a single or multiple amino acid substitution, deletion and/or addition to MCG4 wherein the presence of such a mutation is indicative of or a propensity to develop said condition.

18. A method for detecting MCG4 or a derivative thereof in a biological sample said method comprising contacting said biological sample with an antibody specific for MCG4 or its derivatives or homologues for a time and under conditions sufficient for an antibody-MCG4 complex to form, and then detecting said complex.

19. A method of detecting a condition caused or facilitated by an aberration in *mcg7*, said method comprising determining the presence of a single or multiple nucleotide substitution, deletion and/or addition or other aberration to one or both alleles of said *mcg7* wherein the presence of such a nucleotide substitution, deletion and/or addition or other aberration may be indicative of said condition or a propensity to develop said condition.

20. A method of detecting a condition caused or facilitated by an aberration in *mcg7*, said method comprising screening for a single or multiple amino acid substitution, deletion and/or addition to MCG7 wherein the presence of such a mutation is indicative of or a propensity to develop said condition.

21. A method for detecting MCG7 or a derivative thereof in a biological sample said method comprising contacting said biological sample with an antibody specific for MCG7 or its derivatives or homologues for a time and under conditions sufficient for an antibody-MCG7 complex to form, and then detecting said complex.

22. A method of detecting a condition caused or facilitated by an aberration in *mcg18*, said method comprising determining the presence of a single or multiple nucleotide substitution, deletion and/or addition or other aberration to one or both alleles of said *mcg18* wherein the presence of such a nucleotide substitution, deletion and/or addition or other aberration may be indicative of said condition or a propensity to develop said condition.

23. A method of detecting a condition caused or facilitated by an aberration in *mcg18*, said method comprising screening for a single or multiple amino acid substitution, deletion and/or addition to MCG18 wherein the presence of such a mutation is indicative of or a propensity to develop said condition.

24. A method for detecting MCG18 or a derivative thereof in a biological sample said method comprising contacting said biological sample with an antibody specific for MCG18 or its derivatives or homologues for a time and under conditions sufficient for an antibody-MCG18 complex to form, and then detecting said complex.